

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LEHRER, ROBERT I.
HARWIG, SYLVIA S.L.
KOKRYAKOV, VLADIMIR N.
- (ii) TITLE OF INVENTION: PROTEGRINS
- (iii) NUMBER OF SEQUENCES: 76
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS LLP
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/128,345
 - (B) FILING DATE: 03-AUG-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura, A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 8067-0054-999
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG	48
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp	
1 5 10 15	
CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC	96
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu	
20 25 30	
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG	144
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln	
35 40 45	
TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC	192
Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro	
50 55 60	
AAG GCC GAC GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG	240
Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val	
65 70 75 80	
AAG GAG ACT GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT	288
Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys	
85 90 95	
GAC TTC AAG GAG AAC GGG CGG GTG AAA CAG TGT GTG GGG ACA GTC ACC	336
Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr	
100 105 110	
CTG GAT CAG ATC AAG GAC CCG CTC GAC ATC ACC TGC AAT GAG GTT CAA	384
Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln	
115 120 125	
GGT GTC AGG GGA GGT CGC CTG TGC TAT TGT AGG CGT AGG TTC TGC GTC	432
Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val	
130 135 140	
TGT GTC GGA CGA GGA TGA CGGTTGCGAC GGCAGGCTTT CCCTCCCCCA	480
Cys Val Gly Arg Gly *	
145 150	
ATTTTCCCGG GGCCAGGTTT CCGTCCCCCA ATTTTTCGCG CTCCACCTTT CCGGCCCGCA	540
CCATTCGGGTC CACCAAGGTT CCCTGGTAGA CGGTGAAGGA TTTGCAGGCA ACTCACCCAG	600
AAGGCCTTTC GGTACATTAA AATCCCAGCA AGGAGACCTA AGCATCTGCT TTGCCAGGC	660
CCGCATCTGT CAAATAAATT CTTGTGAAAC C	691

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp
1 5 10 15
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu
20 25 30
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln
35 40 45
Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro
50 55 60
Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val
65 70 75 80
Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys
85 90 95
Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr
100 105 110
Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln
115 120 125
Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val
130 135 140
Cys Val Gly Arg Gly *
145 150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp

48

155										160					165					
CTT	CTG	CTG	CTG	GCA	CTC	GTG	GTG	CCC	TCG	GCC	AGC	GCC	CAG	GCC	CTC	96				
Leu	Leu	Leu	Leu	Ala	Leu	Val	Val	Pro	Ser	Ala	Ser	Ala	Gln	Ala	Leu					
170								175				180								
AGC	TAC	AGG	GAG	GCC	GTG	CTT	CGT	GCT	GTG	GAT	CGC	CTC	AAC	GAG	CAG	144				
Ser	Tyr	Arg	Glu	Ala	Val	Leu	Arg	Ala	Val	Asp	Arg	Leu	Asn	Glu	Gln					
185								190				195								
TCC	TCG	GAA	GCT	AAT	CTC	TAC	CGC	CTC	CTG	GAG	CTG	GAC	CAG	CCG	CCC	192				
Ser	Ser	Glu	Ala	Asn	Leu	Tyr	Arg	Leu	Leu	Glu	Leu	Asp	Gln	Pro	Pro					
200								205				210								
AAG	GCC	GAC	GAG	GAC	CCG	GGC	ACC	CCG	AAA	CCT	GTG	AGC	TTC	ACG	GTG	240				
Lys	Ala	Asp	Glu	Asp	Pro	Gly	Thr	Pro	Lys	Pro	Val	Ser	Phe	Thr	Val					
215								220				225				230				
AAG	GAG	ACT	GTG	TGT	CCC	AGG	CCG	ACC	CGG	CAG	CCC	CCG	GAG	CTG	TGT	288				
Lys	Glu	Thr	Val	Cys	Pro	Arg	Pro	Thr	Arg	Gln	Pro	Pro	Glu	Leu	Cys					
				235								240				245				
GAC	TTC	AAG	GAG	AAC	GGG	CGG	GTG	AAA	CAG	TGT	GTG	GGG	ACA	GTC	ACC	336				
Asp	Phe	Lys	Glu	Asn	Gly	Arg	Val	Lys	Gln	Cys	Val	Gly	Thr	Val	Thr					
				250								255				260				
CTG	GAT	CAG	ATC	AAG	GAC	CCG	CTC	GAC	ATC	ACC	TGC	AAT	GAG	GTT	CAA	384				
Leu	Asp	Gln	Ile	Lys	Asp	Pro	Leu	Asp	Ile	Thr	Cys	Asn	Glu	Val	Gln					
				265								270				275				
GGT	GTC	AGG	GGA	GGT	CGC	CTG	TGC	TAT	TGT	AGG	CGT	AGG	TTC	TGC	ATC	432				
Gly	Val	Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Arg	Arg	Phe	Cys	Ile					
280								285				290								
TGT	GTC	GGA	TGA	GGATGACGGT	TGCGACGGCA	GGCTTTCCT	CCCCCAATTT									484				
Cys	Val	Gly	*																	
295																				
TCCCGGGGCC AGGTTTCCGT CCCCCAATTT TTCCGCCTCC ACCTTTCGG CCCGCACCAT 544																				
TCGGTCCACC AAGGTTCCCT GGTAGACGGA GAGGGATTG CAGGCAACTC ACCCAGAAGG 604																				
CCTTTCGGTA CATTAAATC CCAGCAAGGA GACCTAAGCA TCTGCTTTGC CCAGGCCCGC 664																				
ATCTGTCAAA TAAATTCTTG TGAAACC 691																				

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp
1 5 10 15
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu
20 25 30
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln
35 40 45
Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro
50 55 60
Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val
65 70 75 80
Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys
85 90 95
Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr
100 105 110
Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln
115 120 125
Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Ile
130 135 140
Cys Val Gly *
145

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG 48
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp
150 155 160
CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC 96
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu

165	170	175	180	
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG				144
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln				
	185	190	195	
TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC				192
Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro				
	200	205	210	
AAG GCC GAC GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG				240
Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val				
	215	220	225	
AAG GAG ACT GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT				288
Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys				
	230	235	240	
GAC TTC AAG GAG AAC GGG CGG GTG AAA CAG TGT GTG GGG ACA GTC ACC				336
Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr				
	245	250	255	260
CTG GAT CAG ATC AAG GAC CCG CTC GAC ATC ACC TGC AAT GAG GTT CAA				384
Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln				
	265	270	275	
GGT GTC AGG GGA GGT GGC CTG TGC TAT TGT AGG CGT AGG TTC TGC GTC				432
Gly Val Arg Gly Gly Gly Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val				
	280	285	290	
TGT GTC GGA CGA GGA TGA CGGTTGCGAC GGCAGGCTTT CCCTCCCCCA				480
Cys Val Gly Arg Gly *				
	295			
ATTTTCCCGG GGCCAGGTTT CCGTCCCCCA ATTTTCCGC CTCCACCTTT CCGGCCCCGCA				540
CCATTCGGTC CACCAAGGTT CCCTGGTAGA CGGTGAAGGA TTTGCAGGCA ACTCACCCAG				600
AAGGCCTTTC GGTACATTAA AATCCCAGCA AGGAGACCTA AGCATCTGCT TTGCCCAGGC				660
CCGCATCTGT CAAATAAATT CTTGTGAAAC C				691

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Thr	Gln	Arg	Ala	Ser	Leu	Cys	Leu	Gly	Arg	Trp	Ser	Leu	Trp
1					5				10					15	

Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu
 20 25 30
 Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln
 35 40 45
 Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro
 50 55 60
 Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val
 65 70 75 80
 Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys
 85 90 95
 Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr
 100 105 110
 Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln
 115 120 125
 Gly Val Arg Gly Gly Gly Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val
 130 135 140
 Cys Val Gly Arg Gly *
 145 150

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG	48
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp	
155 160 165	
CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC	96
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu	
170 175 180	
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG	144
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln	
185 190 195	

TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC	192
Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro	
200 205 210	
AAG GCC GAC GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG	240
Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val	
215 220 225 230	
AAG GAG ACT GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT	288
Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys	
235 240 245	
GAC TTC AAG GAG AAC GGG CGG GTG AAA CAG TGT GTG GGG ACA GTC ACC	336
Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr	
250 255 260	
CTG GAT CAG ATC AAG GAC CCG CTC GAC ATC ACC TGC AAT GAG GTT CAA	384
Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln	
265 270 275	
GGT GTC AGG GGA GGT CGC CTG TGC TAT TGT AGG GGT TGG ATC TGC TTC	432
Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe	
280 285 290	
TGT GTC GGA CGA GGA TGA CGGTTGCGAC GGCAGGCTTT CCCTCCCCCA	480
Cys Val Gly Arg Gly *	
295 300	
ATTTTCCCGG GGCCAGGTTT CCGTCCCCCA ATTTTTCGCG CTCCACCTTT CCGGCCCCGCA	540
CCATTCGGTC CACCAAGGTT CCCTGGTAGA CCGTGAAGGA TTTGCAGGCA ACTCACCCAG	600
AAGGCCTTTC GGCACATTAA AATCCCAGCA AGGAGACCTA AGCATCTGCT TTGCCCAGGC	660
CCGCATCTGT CAAATAAATT CTTGTGAAAC C	691

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp
1 5 10 15
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu
20 25 30
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln
35 40 45

Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro
50 55 60

Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val
65 70 75 80

Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys
85 90 95

Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr
100 105 110

Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln
115 120 125

Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe
130 135 140

Cys Val Gly Arg Gly *
145 150

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..198, 603..710, 863..934, 1531..1602)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG	48
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp	
1 5 10 15	
CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC	96
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu	
20 25 30	
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG	144
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln	
35 40 45	
TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC	192
Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro	
50 55 60	
AAG GCC GTGAGTCGGG CAGGGGCTCA GGAGGGGCTG GGGGGCGGGG GCTGTCCCCC	248

Lys Ala
65

ACCCGCCCCG GGGCTCCCTG TCCCTCCCCC TGCTCAGGCT GTCCCTCCTG CCAGGAAGGC	308
ACTTGTCCTT CTAAGGGGGA CCCCCTCTGC CAGGAAACCT TCCCAGAGCT GGGTGCCCTG	368
CCCGCGTGAG AGCTTCCCGC CTTAGCCTCT GGGCTGTGGG CTCAGGGCCC TGCACAGCCT	428
GTGAGGCAGG AGCGGGCTCT GTCCCCCTCC CTGTGCACCC AGCACCAAGC CCAGGGCCAG	488
GCTCCCAGCA GGGGCTGCAG AGGCTGCTGT CTAGGTGGGG GCGGGGAGGG GGTGACAGAT	548
CCGAGGGGGA AGCCTGAGCC CGAGTCCCAT CTCCCCACTT TGATCCTTGA CCAG GAC Asp	605
GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG AAG GAG ACT Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val Lys Glu Thr 70 75 80	653
GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT GAC TTC AAG Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys Asp Phe Lys 85 90 95	701
GAG AAC GGG GTGAGGCTGG GGGCTGGGGG CGCTGGCGGA TGCTTCCCAA Glu Asn Gly 100	750
GGAGCTGAAC AGGAGAGCCT GCTGGGGAAG ATGTCCAGGC CCTGGGGTGA GGCTGGGAGC	810
TCATGGATGG AGGAGGGGGG GTCCCAGTTT GACCTTGAGT CTCCCCTTCC AG CGG Arg	865
GTG AAA CAG TGT GTG GGG ACA GTC ACC CTG GAT CAG ATC AAG GAC CCG Val Lys Gln Cys Val Gly Thr Val Thr Leu Asp Gln Ile Lys Asp Pro 105 110 115	913
CTC GAC ATC ACC TGC AAT GAG GTGAGTGGCC CCTTATTGGT GTCAAGTTGC Leu Asp Ile Thr Cys Asn Glu 120 125	964
TAATGGGTTG GTGTGGGGAA CTCCTTGGA GTGTTACCCG CTGCCCCATC CAGGGCGTGG	1024
AAAGGCCCTC CTACCCCGGC CCTTCCCTCA CCTCGGCCCC AGGGCTCCAG GTCTGGCTCT	1084
GTCATCCTTA GGGCCGCGGT TCCCTCAATG GGGTCCCCC CTCGTATTG TCAGAAAGGC	1144
ACATTTTCAGG CCCCACCCCG ACCCTCTGAA TCACACTCTT GGGTGGAGCC CAGCCTTGTC	1204
TCTTCTCCCA AGATCCCAGC GGGTTCTTCC TGTGCTGTCT GCTGAGAGGC AGTGACCGGA	1264
CTAATGGACT TGCAGGCCCT GCTCCTGGCC AGCTTTGCGG GGCTGGGTTT GGGACCCTGG	1324
CAAGGCCCCA GCCATCTCTG GGCCTGAGTC CACTTATGTG TCTGTGGGGG ATTCCACCAC	1384

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Gly Gly Gly Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Phe Phe Arg Leu Cys Tyr Cys Arg Pro Arg Phe Cys Val Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Ile Cys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Gly Gly Gly Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Pro Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "homoarginine(Har) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Gly Gly Xaa Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: group(4, 9)
(D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg Gly Gly Xaa Leu Cys Tyr Cys Xaa Arg Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Arg Gly Gly Arg Val Cys Tyr Cys Arg Xaa Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Lys Lys Trp Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Xaa	Arg	Tyr	Cys	Val	Cys	Val
1				5					10					15	

Gly Arg

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Arg	Gly	Ser	Gly	Leu	Cys	Tyr	Cys	Arg	Arg	Lys	Trp	Cys	Val	Cys	Val
1				5					10					15	

Gly Arg

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Ala Thr Arg Ile Cys Phe Cys Arg Arg Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Gly Gly Lys Val Cys Tyr Cys Arg Xaa Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "D-form of amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Arg Ala Thr Arg Ile Cys Phe Cys Arg Arg Arg Phe Cys Val Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har)"
 /note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Arg Gly Gly Lys Val Cys Tyr Cys Arg Xaa Arg Phe Cys Val Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "All D-form amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:34:

(ix) **FEATURE:**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

(2) INFORMATION FOR SEO ID NO:35:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Arg

(2) INFORMATION FOR SEQ ID NO:36:

(ix) **FEATURE:**

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(B) LOCATION: 1..18
(D) OTHER INFORMATION: /note= "All D-form amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Gly Gly Arg Leu Val Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Gly Gly Arg Leu Gly Tyr Cys Arg Arg Arg Phe Cys Ile Cys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY. linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Arg Gly Gly Gly Leu Cys Tyr Gly Arg Arg Arg Phe Cys Val Cys Val
1 5 10 15
Gly Arg

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Arg Gly Gly Arg Leu Gly Tyr Gly Arg Arg Arg Phe Gly Val Cys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Lys Gly Gly Arg Leu Val Tyr Val Arg Arg Arg Phe Ile Val Cys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 4

(D) OTHER INFORMATION: /product= "homoarginine(Har) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Arg	Gly	Gly	Xaa	Leu	Cys	Tyr	Cys	Arg	Arg	Arg	Phe	Cys	Val	Gly	Val
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: group(4, 9)

(D) OTHER INFORMATION: /product= "homoarginine(Har) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Arg	Gly	Gly	Xaa	Leu	Cys	Tyr	Cys	Xaa	Arg	Arg	Phe	Cys	Val	Leu	Val
1				5				10						15	

Gly Arg

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /product= "homoarginine(Har) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Arg Gly Gly Arg Val Cys Tyr Val Arg Xaa Arg Phe Leu Val Gly Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Gly Gly Arg Leu Cys Tyr Ser Arg Lys Lys Trp Cys Val Ser Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Xaa Arg Tyr Ser Val Val Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Arg Gly Ser Gly Leu Ser Tyr Cys Arg Arg Lys Trp Gly Val Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Arg Ala Thr Arg Ile Ser Phe Ser Arg Arg Arg Phe Ser Val Ser Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Arg Gly Gly Lys Val Cys Tyr Gly Arg Xaa Arg Phe Ser Val Cys Val
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(9, 18)
- (D) OTHER INFORMATION: /note= "D form of amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Arg	Ala	Thr	Arg	Ile	Val	Phe	Cys	Arg	Arg	Arg	Phe	Gly	Val	Cys	Val
1				5				10					15		

Gly Arg

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION: /product= "homoarginine(Har)"
- /note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg	Gly	Gly	Lys	Val	Cys	Tyr	Leu	Arg	Xaa	Arg	Phe	Leu	Val	Cys	Val
1			5					10					15		

Gly Arg

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg	Gly	Gly	Arg	Ile	Cys	Phe	Leu	Arg	Pro	Arg	Ile	Gly	Val	Cys	Val
1				5					10					15	

Gly Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 8..13

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Arg	Gly	Gly	Arg	Leu	Xaa	Tyr	Cys	Arg	Arg	Arg	Phe	Cys	Val	Xaa	Val
1				5					10					15	

Gly Arg

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 8..13

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Arg Gly Gly Arg Leu Xaa Tyr Cys Arg Arg Arg Phe Cys Ile Xaa Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 8..13

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Arg Gly Gly Gly Leu Xaa Tyr Cys Arg Arg Arg Phe Cys Val Xaa Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 8..13

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Gly Gly Arg Leu Xaa Tyr Cys Arg Trp Gly Ile Cys Phe Xaa Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 8..13

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Arg Gly Gly Arg Leu Xaa Tyr Cys Arg Pro Arg Phe Cys Val Xaa Val
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Disulfide-bond
 (B) LOCATION: 6..15

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: group(8, 13)
 (D) OTHER INFORMATION: /note= "X is a hydrophobic, a
small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Xaa	Arg	Arg	Arg	Phe	Xaa	Val	Cys	Val
1				5				10						15	

Gly Arg

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Disulfide-bond
 (B) LOCATION: 6..15

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: group(8, 13)
 (D) OTHER INFORMATION: /note= "X is a hydrophobic, a
small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Xaa	Arg	Arg	Arg	Phe	Xaa	Ile	Cys	Val
1				5				10						15	

Gly Arg

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 6..15

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(8, 13)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Xaa	Arg	Pro	Arg	Phe	Xaa	Val	Cys	Val
1				5				10					15		

Gly Arg

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 8, 13, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Arg	Gly	Gly	Arg	Leu	Xaa	Tyr	Xaa	Arg	Arg	Arg	Phe	Xaa	Val	Xaa	Val
1				5				10					15		

Gly Arg

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: group(6, 8, 13, 15)
 (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Arg	Gly	Gly	Arg	Leu	Xaa	Tyr	Xaa	Arg	Arg	Arg	Phe	Xaa	Ile	Xaa	Val
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: group(6, 8, 13, 15)
 (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Arg	Gly	Gly	Gly	Leu	Xaa	Tyr	Xaa	Arg	Arg	Arg	Phe	Xaa	Val	Xaa	Val
1				5				10					15		

Gly Arg

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: group(5, 7, 13, 15)
 (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTCGTCTAGA SGTTCACAA GAATTTATTT

30

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Gly	Trp	Ile	Cys	Phe	Cys	Val
1				5					10					15	

Gly Arg Gly

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGGCCGTGA GTCG

14

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AACGGGGTGA GGCT

14

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AATGAGGTGA GTGG

14

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTGACCAGGA CGAG

14

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCTTCCAGCG GGTG

14

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGTCACAGGT TCAA

14